EXHIBIT 2

```
########################################
# Program:  needle
# Rundate:  Mon Jul 31 07:00:44 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-0700432328664.output
########################################

#=======================================
#
# Aligned_sequences: 2
# 1: SEQ173
# 2: G_kaustophilus
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1138
# Identity:     987/1138 (86.7%)
# Similarity:   987/1138 (86.7%)
# Gaps:         147/1138 (12.9%)
# Score: 5832.0
#
#=======================================
```

SEQ173   1   aattccgac   9
                                                             .||||||||
G_kaustophil   101 aactaacagcaaccgcctcgggagtaacgctgaccggaagcgattccgac   150

SEQ173   10 atttcaattgaatcgtttattccgcttgaaaaagaaggcaagttgctcgt   59
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil   151 atttcaattgaatcgtttattccgcttgaaaaagaaggcaagttgctcgt   200

SEQ173   60 tgatgtgaaaagaccggggagcatcgtactgcaggcgcgctttttctctg   109
                      |||·|||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil   201 tgacgtgaaaagaccggggagcatcgtactgcaggcgcgctttttctctg   250

SEQ173   110 aaatcgtgaaaaaactgccgcaacaaacggtggaaatcgaaacggaagac   159
                      |||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil   251 aaatcgtgaaaaaactgccgcaacaaacggtggaaatcgaaacggaagac   300

SEQ173   160 aacttttttgacgatcatccgctcggggcactcagaattccgcctcaatgg   209
                      |||||·|||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil   301 aacttttttgacgatcatccgctcggggcactcagaattccgcctcaatgg   350

SEQ173   210 gctaaacgccgacgaatatccgcgcctgcgcaaatgaagaagaaaacg   259
                      |||||||||||||||||||||||||||||||||||·|||||||||||||
G_kaustophil   351 gctaaacgccgacgaatatccgcgcctgcgcaaatgaagaagaaaacg   400

SEQ173   260 tgtttcaaatcccggctgatttattgaaaaccgtgattcggcaaacggtg   309
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil   401 tgtttcaaatcccggctgatttattgaaaaccgtgattcggcaaacggtg   450

SEQ173   310 ttcgccgtttctacatcggaaacgcgcccaatcttgacaggtgtcaactg   359
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil   451 ttcgccgtttctacatcggaaacgcgcccaatcttgacaggtgtcaactg   500

SEQ173   360 gaaagttgaacatggcgagcttgtctgcacagccgaccgacagtcatcgct   409
                      ||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil   501 gaaagttgaacatggcgagcttgtctgcacagccgaccgacagtcatcgct   550

```
SEQ173        410 tagccatgcgcaaagtgaaaattgagtcggaaaatgaagtatcatacaac    459
                  ||:||:||||::|:||:||||||:|:||:|||:||:::|||:||:||::||
G_kaustophil  551 tagccatgcgcaaagtgaaaattgagtcggaaaatgaagtatcatacaac    600

SEQ173        460 gtcgtcatccctggaaaaagtcttaatgagctcagcaaaattttggatga    509
                  ||||||:||:|||||||||||||||||||||||||||||||:|:||||||
G_kaustophil  601 gtcgtcatccctggaaaaagtcttaatgagctcagcaaaattttggatga    650

SEQ173        510 cggcaaccacccggtggacatcgtcatgcagccaatcaagtgctattta    559
                  ||||||||||||:||:||||:|:||||||||||||||||:|||||||||
G_kaustophil  651 cggcaaccacccggtggacatcgtcatgcagccaatcaagtgctattta    700

SEQ173        560 aggccgagcaccttctcttctttttcccggctgcttgacggcaactatccg    609
                  |||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil  701 aggccgagcaccttctcttctttttcccggctgcttgacggcaactatccg    750

SEQ173        610 gagacggcccgcttgattccaacagaaagcaaaacgaccatgatcgtcaa    659
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil  751 gagacggcccgcttgattccaacagaaagcaaaacgaccatgatcgtcaa    800

SEQ173        660 tgcaaaagagtttctgcaggcaatcgaccgagcgtccttgcttgctcgag    709
                  |:|||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil  801 tacaaaagagtttctgcaggcaatcgaccgagcgtccttgcttgctcgag    850

SEQ173        710 aaggaaggaacaacgttgtgaaactgacgacgcttcctggaggaatgctc    759
                  |||||||||||||||||||||||||||||||||-|||||||||||||||||
G_kaustophil  851 aaggaaggaacaacgttgtgaaactaacgacgcttcctggaggaatgctc    900

SEQ173        760 gaaatttcttcgatttctcc-gagatcgggaaagtgacggagcagctgca    808
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil  901 gaaatttcttcgatttctccggagatcgggaaagtgacggagcagctgca    950

SEQ173        809 aacggagtctcttgaaggggaagagttgaacatttcgttcagcgcgaaat    858
                  ||||||||||||||||||||||||||||||||||||||||||||||||||
G_kaustophil  951 aacggagtctcttgaaggggaagagttgaacatttcgttcagcgcgaaat    1000

SEQ173        859 atatgatggacgcgttgcgggcgcttgatggaacagacatttcaaatcag    908
                  |||||||||||||||||||||||||||||||||||||||| |||||||||
G_kaustophil  1001 atatgatggacgcgttgcgggcgcttgatggaacagaca-ttcaaatcag    1049

SEQ173        909 cttcactggggccatgcggccgttcctgttgcgcccgcttca-accgatt    957
                  |||||||||||||||||||||||||||||||||||||||||| |||||||
G_kaustophil  1050 cttcactggggccatgcggccgttcctgttgcgcccgcttcataccgatt    1099

SEQ173        958 cgatgcttcagctcattttgccggtgagaacatat          992
                  |||||||||||||||||||||||||||||||||||
G_kaustophil  1100 cgatgcttcagctcattttgccggtgagaacatattga       1137
```

```
#########################################
# Program:  needle
# Rundate:  Mon Jul 31 07:01:59 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07015859433755.output
#########################################

#=======================================
#
# Aligned_sequences: 2
# 1: SEQ173
# 2: B_cereus
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1146
# Identity:    654/1146 (57.1%)
# Similarity:  654/1146 (57.1%)
# Gaps:        160/1146 (14.0%)
# Score: 3294.5
#
#=======================================

SEQ173            1                                     aattccgac      9
                                                        .||.|.||.
B_cereus        101 aggttgtagctacggaagaaggagttacattaacaggaagcgatgctgat    150

SEQ173           10 atttcaattgaatcgtttattccgcttgaaaaagaagcaagttgctcgt     59
                    |||||.||||||||.|||||.||..|||||.|||||||.|.||...|||
B_cereus        151 atttcgattgaatctttatcccagttgaagaggatggaaaagaaatcgt    200

SEQ173           60 tgatgtgaaaagaccgggggagcatcgtactgcaggcgcgcttttttctctg    109
                    .||.|.|||.|.|.|.|||.|.|||||.....||||||...|||||...||
B_cereus        201 agaagtaaacaatcaggaagtattgtttttacagcggaaatattttagtg    250

SEQ173          110 aaatcgtgaaaaaactgccgcaacaaacggtggaaatcgaaacggaagac    159
                    ||||.||.|||||||.|.|.||..||.|||||.||.||||......|||.|.
B_cereus        251 aaattgtaaaaaaattacctaaagaaactgtagaaatttctgtggaaaat    300

SEQ173          160 aacttttttgacgatcatccgctcggggcactcagaattccgcctcaatgg    209
                    .|.|||..||||.|.||..||.....||.|.|..|||||||||.....|||||
B_cereus        301 catttgatgacaaaaataacttctggaaaatcagagtttaatttaaatgg    350

SEQ173          210 gctaaacgccgacgaatatccgcgcctgccgcaaatgaagaagaaaacg    259
                    ..||.|..|.|..||||||||.||||||||...||.|.|.|.|||.|.|.|
B_cereus        351 tttagattctgcagaatatccgttgttaccacaaattgaagaacatcatg    400

SEQ173          260 tgtttcaaatcccggctgatttattgaaaaccgtgattcggcaaacggtg    309
                    |.|||.|||||||..|.|||||||.||.|||||.|.|.||.|.||.|||.|.
B_cereus        401 tttttaaaatcccaacggatttacttaaacatatgatcagacaaactgta    450

SEQ173          310 ttcgccgtttctacatcggaaacggcgcccaatcttgacaggtgtcaactg    359
                    ||.|.|.||||.|.|.|.|||.|.|..|.|||.|.||||||||||||.....||
B_cereus        451 tttgcagtttccacttctgaaacaagaccgatcttgacaggtgtaaactg    500

SEQ173          360 gaaagttgaacatggcgagcttgtctgcacagcgaccgacagcatcgct    409
                    |||.||.|..|.|.|.||||||.||...||||||.|.||.|..|.||.|.|
B_cereus        501 gaaggtatataacagcgaactaacttgcattgctacagatagccacagt    550
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SEQ173       410 tagccatgcgcaaagtgaaaartg agtcg--gaaatgaagtatcatac  456
                 |||| .|.|.|||.||||.. |||.| .|.||||| ..||..|
B_cereus     551 tagctcttcgadaagcaaaatcgaaggcattgcagatgaa-ttccagc    599

SEQ173       497 aac-gtcgtcatccctggaaaaagtcttaatgagctcagcaaaattttgg  505
                 ||. ||.|.|||.|||||.|.|.|||||..|.|||.|...|.||||||||||
B_cereus     600 aaatgttgttatcccagggaaaagcttaaatgaattaagcaaaattttag  649

SEQ173       506 atga--cggcaaccacccggtggacatcgtcatgacagccaatcaagtgc  553
                 |||| |.|.|. |...|||.||||||.||.||.|....|||||..
B_cereus     650 atgagtctgaag--aaatggtagatatcgttattacggagtatcaagtat  697

SEQ173       554 tatttaaggccgagcaccttctcttctttcccggctgcttgacggcaac  603
                 |||||....|||||||.||..|.||..|||||.||.|.|||||..||.|
B_cereus     698 tattccgtacaaaacattattattcttctcaagattgttagaaggaaat  747

SEQ173       604 tatccggagacggcccgcttgattccaacagaaagcaaaacgaccatgat  653
                 |||||.||.|||||.||.||.|.|||||.|.|||||.||||||..|.|
B_cereus     748 tatcctgatacaactcgcttaattccagcggagagtaaaacagatatttt  797

SEQ173       654 cgtcaatgcaaaagagtttctgcaggcaatcgaccgagcgtccttgcttg  703
                 .|.|||.||||||.||||||.|.||||||.||.|.|.||.|.|.|||.||
B_cereus     798 tgtaaatacaaaagaattttacaagcaattgatcgtgcatccctattag  847

SEQ173       704 ctcgagaaggaaggaacaacgttgtgaaactgacgacgcttcctggagg-  752
                 |..||||.||..|.|.|.|.|.|||||.|||.|||.||.|| .|||||
B_cereus     848 caagagatggtcgtaataatgttgtaaaattatcaac-tttagagcaggc  896

SEQ173       753 aatgctcgaaatttcttcgatttctcc-gagatcgggaaagt-gacggag  800
                 ||||||.|||||||||||.||||||.|| |||.||||||.||||| ||.||
B_cereus     897 aatgctagaaatttcttcaaattcaccagaaatcgggaaagtagtagaag  946

SEQ173       801 cagctgcaaacggagtctcttgaagggggaagagttgaacatttcgttcag  850
                 .||.| |||...|.....|.||||.||||||||||||||.||||.||||||
B_cereus     947 aagtt-caatgtgaaaagtagatgggagaagagttaaaaatatctttag  995

SEQ173       851 cgcgaaatatatgatggacgcgttgcgggcgcttgatggaacagacattt  900
                 .|.||||||||||.||.||.||.||||.|...|.|.|..||.|.||.||||
B_cereus     996 tgcaaaatatatgatggatgcactaaaggcattagatagtactgaga-tt 1044

SEQ173       901 caaatcagcttcactggggccatgcgcgccgttcctgttgcgcccgcttca  950
                 .|.||.|||||.||||.|.|.||||.||.|.|..|.|.||.|.|.|..|.|
B_cereus    1045 aagattagcttactggagcaatgagaccatttcttaattcgtacggtaaa 1094

SEQ173       951 -accgattcgatgcttcagctcattttgccggtgagaacatat       992
                 ...|.|.||..||..|||||.||||||.||||.||||..|.||.||.
B_cereus    1095 tgatgaatccattattcaattaatttaccggttcgtacttactaa    1140
```

```
####################################
# Program:  needle
# Rundate:  Mon Jul 31 07:03:18 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07031637746308.output
####################################

#=======================================
#
# Aligned_sequences: 2
# 1: SEQ173
# 2: B_thuringiensis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1148
# Identity:     655/1148 (57.1%)
# Similarity:   655/1148 (57.1%)
# Gaps:         164/1148 (14.3%)
# Score: 3260.0
#
#=======================================
```

```
SEQ173             1                                              aattccgac         9
                                                                  .||.|.||.
B_thuringiens    101 aagttgtcgctacggaagaaggagttacattaacaggaaagcgatgctgat       150

SEQ173            10 atttcaattgaatcgtttattccgcttgaaaaagaaggcaagttgctcgt        59
                     |||||.||||||||.||||.||.|||||.|||.|||||.|||.|.|||||.||
B_thuringiens    151 atttcgattgaatctttatcccagttgaagaggatggaaaagaaattgt       200

SEQ173            60 tgatgtgaaaagaccggggagcatcgtactgcaggcgcgcttttctctg       109
                     .|||.|||||||.|.|.||||||.|.|||.|.|||.|||||.|.|||..||
B_thuringiens    201 agaagtaaaacaatcaggaagtattgtttacaggctaaatatttagtg       250

SEQ173           110 aaatcgtgaaaaaactgccgcaacaaacggtggaaa--tcgaaacggaag       157
                     |||||.||.|||||.|||||.||||.||.|.|||||.||||  ...||.||
B_thuringiens    251 aaattgtaaaaaaattgccgaaagaaactgtagaaatttc-tgtcgaaaa       299

SEQ173           158 acaacttttttgacgatcatccgctcggggcactcagaattccgcctcaat       207
                     .||.  ||..|||.|.|...|....||.|||.|||.|.....|||
B_thuringiens    300 tcat-ttaatgacaaaaataacttctgggaaatcagaatttaatttaaat       348

SEQ173           208 gggctaaacgccgacgaatatccgcgcctgccgcaaattgaagaagaaaa       257
                     ||..|||.||..|.|.|||||||.|||||.....|.||||||||||||||
B_thuringiens    349 ggttagattctgcagaatatccattgttaccacaaattgaagaacatca       398

SEQ173           258 cgtgtttcaaatcccggctgatttattgaaaaccgtgattcggcaaacgg       307
                     .||||.||.|.|.|.|||.||||||||.|.||||||.|.||.||||||||
B_thuringiens    399 tgttttttaagattccaacagatttacttaaacatatgatcagacaaactg       448

SEQ173           308 tgttcgccgtttctacatcggaaacgcgccaaatcttgacaggtgtcaac       357
                     |.|.|.||.||.||.|.||.||.||.|.|..|.|||||||||||||||||
B_thuringiens    449 tatttgcagtctccacttctgaaacaagaccaatcttgacaggtgtaaac       498

SEQ173           358 tggaaagttgaacatggcgagcttgtctgcacagcgaccgacagtcatcg       407
                     ||||.|.|..|.|.|..||..||.||.|.|||.|.||.||||||.||||||
B_thuringiens    499 tggaaggtatataacagcgaactaacttgtattgctacagatagtcacag       548
```

```
SEQ173        408 cttagccatgcgcaaagtgaaaattga--gtc-ggaaaatgaagtatcat      454
                  .:||||.-|.|:|.|||:-.:||||||||   |:. -|.|.|||:; ;-.|.
B_thuringiens 549 gttagctcttcgaaaagcaaaaattgaaggtattgtagatgaa-ttccag      597

SEQ173        455 acaac-gtcgtcatccctggaaaaagtcttaatgagctcagcaaaattt      503
                  .:|||.  :|.|:.;|.|||-.|.||.|||:|..:|||||..:.|:|:|||||:.|
B_thuringiens 598 gcaaatgttgttattccgggaaaagcttaaatgaattaagcaaaattct      647

SEQ173        504 ggatga--cggcaaccacccggtggacatcgtcatgacagccaatcaagt      551
                  .:|||||  .|.|-.|   .-:||.||-|||:|:|.:|:|.||||.....|||||||
B_thuringiens 648 agatgagtctgaag--aaatggtaagatatcgttattacggagtatcaagt      695

SEQ173        552 gctatttaaggccgagcacccttctcttctttttcccggctgcttgacggca      601
                  .:|||.....|.:||||-.|.|..|.||||||..:||||.....||.|.|.||.|
B_thuringiens 696 attattccgtacaaaacatttattattcttctcaagattgttagaagaa      745

SEQ173        602 actatccggagacggccgcttgattccaacagaaagcaaaacgaccatg      651
                  |.:||||.||.:|.-.|.:||.|.||||...:.||||||.|.|||||||||:|
B_thuringiens 746 attatcctgatacaactcgattaattcctgcagagagtaaaacagatatt      795

SEQ173        652 atcgtcaatgcaaaagagtttctgcaggcaatcgaccgagcgtccttgct      701
                  .:.:|.|||.||||||:.||:|.||.:|||||.|.||.|:.||.||.:.|.:|
B_thuringiens 796 tttgtaaatacaaaagaattttacaagtgatcgtgcatcrctgtt      845

SEQ173        702 tgctcgagaaggaaggaacaacgttgtgaaactgacgacgcttcctggag      751
                  .:||.||||.||.-.:|.|:|-.:||.|||||||||||||:|..:.||  .||.|:|
B_thuringiens 846 agctagagatggtcgtaataatgttgtgaaattatcaac-tttagagcag      894

SEQ173        752 g-aatgctcgaaatttcttcgatttctcc-gagatcgggaaagt-gacgg      798
                  | ||||||.|||||||||||||||||.||.  -.||:|||||||||||||:.|.
B_thuringiens 895 gcaatgctagaaatttcttcgaattcaccagaaatcgggaaagtagtaga      944

SEQ173        799 agcagctgcaaacggagtctcttgaaggggaagagttgaacatttcgttc      848
                  ||.|.|.||| ||...:||.....:|.||:||.-.|:||.||||.|||||||
B_thuringiens 945 agaagtt-caatgtgaaaaagtagatgggagaagagttaaaaatatctttt      993

SEQ173        849 agcgcgaaatatatgatggacgcgttgcgggcgcttgatggaacagacat      898
                  ||-.||.-|.||||||||||||.:||.||-...:|||...|.||||.:.|.:|| |-.
B_thuringiens 994 agtgcaaatatatgatggatgcactaaaggcattagatagtactga-aa     1042

SEQ173        899 ttcaaatcagcttcactggggccatgcggccggttcctgttgcgcccgctt      948
                  :|.|-.|||.|||||.|||||.:|-|:.|||.|.:|:.||.:.||:|.||-.|.
B_thuringiens 1043 ttaagattagctttactggagcaatgagaccacattcttaattcgtacggca     1092

SEQ173        949 ca-accgattcgatgcttcagctcattttgccggtgagaacatat       992
                  .:  ...:||.||.:||...:|||||..:.||||||.|.||||:||.:|.||..
B_thuringiens 1093 aatgatgaatccattattcaattaattttaccggttcgtacttactaa     1140
```

```
##########################################
# Program:  needle
# Rundate:  Mon Jul 31 07:04:20 2006
# Align_format: srspair
# Report_file: /ebl/wxfserv/old-work/needle-20060731-07041940078774.output
##########################################

#=======================================
#
# Aligned_sequences: 2
# 1: SEQ173
# 2: B_weihenstephanensis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1149
# Identity:     636/1149 (55.4%)
# Similarity:   636/1149 (55.4%)
# Gaps:         160/1149 (13.9%)
# Score: 3242.0
#
#=======================================
```

SEQ173   1   aattccgac   9
                                                          .|.|.|||
B_weihensteph   101 aagttgtagcaactgaagaaggagttactttaacaggtagtgatgcagac   150

SEQ173   10 atttcaattgaatcgtttattccgcttgaaaaagaaggcaagttgctcgt   59
                       ||.||.||.|||.|||||.|||||.||..|.|||.|.|.|||.||.....|.||
B_weihensteph   151 atctctatcgaatcatttatcccagtcgaagatgctggaaagaaaattgt   200

SEQ173   60 tgatgtgaaaagaccggggagcatcgtactgcaggcgcgcttttctctg   109
                      .||..|..||..|.|.|.||.|.||..|.|.|.||...|.|.|||..||
B_weihensteph   201 ggaaattgaacaatcaggaagtattattttacaagcaaaatattttagtg   250

SEQ173   110 aaatcgtgaaaaaactgccgcaacaaacggtggaaatcgaaacggaagac   159
                      |.|||||.|||||.||||.||.||..||.||.|||.||.|||.|.|.|.|.
B_weihensteph   251 agatgctgaaaaaattaccctaaagaaactgtcgaaatttctgtgtgaaaat   300

SEQ173   160 aacttttttgacgatcatccgctcggggcactcagaattccgcctcaatgg   209
                      .|.|||.|||||.||.||....||||..||||||.|.||||.||....|.|.||
B_weihensteph   301 cattttatgacaaaaataaaatctggaaatcagagttcaacttaaatgg   350

SEQ173   210 gctaaacgccgacgaatatccgcgcctgccgcaaattgaagaagaaaacg   259
                      ..||.|.|||.|.|.||||||||....|.||.|||||.||.|||||.|..|.|
B_weihensteph   351 tttagatgctgctgaatatccgttattaccacaaatcgaagaacatcatg   400

SEQ173   260 tgtttcaaatcccggctgatttattgtgaaaaccgtgattcggcaaacggtg   309
                      |.|||.|.|.|.|..|.|||||.|.||..|.|.||||||.|.||||.||||.|.
B_weihensteph   401 tatttaaggattccaacagatttactaaagcacatgattcgtcaaacagta   450

SEQ173   310 ttcgccgtttctacatcggaaacgcgcccaatcttgacaggtgtcaactg   359
                      ||.||.||.|||.|..|.||.|||||||..||.|||.'||||||||||.||||
B_weihensteph   451 tttgcagtttcaagttctgaaacaagaccgatcttgacaggtgtaaactg   500

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10066505.1
```

```
SEQ173        360 gaaaagttgaacatggcgagcttgtctgcacagccgaccgacagtcatcgct       409
                  .|||.||...|...|||||||...|..||||.||.|.||.||||...|...
B_weihensteph 501 gaaggtagtatagcagcgagctaacttgtattgcaacagatagtcacagac      550

SEQ173        410 tagccatgcgcaaagtgaaaattga---gtcggaaaatgaag-----tat       451
                  ||||..|.||.|||.||||..||||||   ||.....||..|    .||
B_weihensteph 551 tagcaacttcgtaaagcaaaaatcgaagggtataatattgccgatgaattt      600

SEQ173        452 catac-aacgtcgtcatccctggaaaaagtcttaatgagctcagcaaaat       500
                  ||..| |.|||||.|.||||||.||.||||||.||.|....|||...|.|||||||
B_weihensteph 601 caagcgaatgtcgttattcctggtaagagcttaagtgaattaagtaaaat      650

SEQ173        501 tttggatga--cggcaaccacccggtggacatcgtcatgacagccaatca       548
                  |.|.||||| |.|.. |...|||.||.||||||.||.|.||..|....||||
B_weihensteph 651 tctagatgaatctgaag--aaatggtagatatcgttattacggagtatca      698

SEQ173        549 agtgctatttaaggccgagcacctctctcttttccccggctgcttgacg       598
                  |||..|||.....|.|.||.||..|.|||||.||.|..|.....|.||.|
B_weihensteph 699 agtattattccgtacaaaacatttattattcttctcacagattacgaagagag      749

SEQ173        599 gcaactatccggagacggccggccgcttgattccaacagaaagcaaaacgacc       648
                  |.||.|||||.||.||.||..|.||.|.||||.|||||||.|.||||||.....
B_weihensteph 749 gaaattatccagatacaacgcgtttaattccagctgaaagtaaaactgat      798

SEQ173        649 atgatcgtcaatgcaaaagagtttctgcaggcaatcgaccgagcgtcctt       698
                  ||..|..||.||.|.|||.||||.||..|||||.||..|..|.|..|.|.|
B_weihensteph 799 atatttgtaaatacaaaagaattttttacaagcgattgatcgtgcgtcgtt      848

SEQ173        699 gcttgctcgagaaggaaggaacaacgttgtgaaactgacgacgcttcctg       748
                  |.|.|.||||||.||.||.|..|.||||.|.|...||...|.|.|.|....
B_weihensteph 849 gttagcaagagatggtcgtaacaacgttgttaaattatcgacattagaac      898

SEQ173        749 gaggaatgctcgaaatttcttcgatttctcc-gagatcgggaaagtgacg       797
                  .|....||.||.|.||||.||||||||||||.||||.!! ||.|||||.|||||....
B_weihensteph 899 aacagatgttagagatttcttcgaatgcaccagaaatcggaaaagtagta      948

SEQ173        798 gagcagctgcaaacggagtctcttgaaggggaagagttgaacatttcgtt       847
                  ||...|.|.||..|.....||...|.|.|.|.|.|||||||.|||.....||.|
B_weihensteph 949 gaagaggttcaatgtgaaaatgtagatgggagaagaattaaaaatatcttt      998

SEQ173        848 cagcgcgaaatatatgatggacgcgttgcgggcgcttgatggaacagaca       897
                  .||.||.||||||||||||||.|||..||....|...|.||.|||||| |
B_weihensteph 999 tagtgcaaaatatatgatggacgcattaaaggcttttagacagtacaga-a    1047

SEQ173        898 tttcaaatcagcttcactggggccatgcggccggttcctgttgcgcccgct       947
                  .||.||.|.||.||.||||||.||.|||..|.|.||.....||.||||..||.|
B_weihensteph 1048 attaaagttagttttactggagcgatgagaccgtttttaattcgcacagt    1097

SEQ173        948 tca-accgattcgatgcttcagctcattttgccggtgagaacatat         992
                  ..| ...|||||.|||..|..|.||.||.||||||||.||.|.|.||.
B_weihensteph 1098 aaatgatgattccattatccaattaattttaccagtccgtacttactaa     1146
```

```
##################################################
# Program:  needle
# Rundate:  Mon Jul 31 07:06:37 2006
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20060731-07063643205179.output
##################################################

#=======================================
#
# Aligned_sequences: 2
# 1: SEQ173
# 2: B_subtilis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1145
# Identity:     682/1145 (59.6%)
# Similarity:   682/1145 (59.6%)
# Gaps:         161/1145 (14.1%)
# Score: 3577.5
#
#=======================================

SEQ173            1                                         aattccgac          9
                                                            .|.||.||.
B_subtilis      101 aaattgttgcatcagatgatggagtatcctttacagggagtgactcagat        150

SEQ173           10 atttcaattgaatcgtttattccgcttgaaaaagaagcaagttgctcgt         59
                    |||||.|||||||.|||.||.||||....|||.||.||.||....||||
B_subtilis      151 atttctattgaatccttcattccaaaagaagaaggagataaagaaatcgt        200

SEQ173           60 tgatg-tgaaaagaccggggagcatcgtactgcaggcgcgctttttctct        108
                    ...|.|||||.||.||.|||||||..|.|||||.||||||||||...|
B_subtilis      201 cactattgaacagccc-ggaagcatcgttttacaggctcgctttttttagt        249

SEQ173          109 gaaatcgtgaaaaaactgccgcaacaaacggtggaaatcgaa-acggaag        157
                    |||||.||.||.||||||.|||||.....|||.||.||||||.|||..||..
B_subtilis      250 gaaattgtaaaaaaattgccgatggcactgtagaaattgaagtccaaaa        299

SEQ173          158 acaactttttgacgatcatccgctcggggcactcagaattccgcctcaat        207
                    .||.||.||||||.||||.||||.|.||.||.|||||....||.||.
B_subtilis      300 tcag-tatttgacgattatccgttctggtaaagctgaatttaatctaaac        348

SEQ173          208 gggctaaacgccgacgaatatccgcgcctgccgcaaatgaagaagaaaa        257
                    ||.||.|.|.||.|||||||||||||.||||.|.||||||.|.|..|
B_subtilis      349 ggactggatgctgatgaatatccgcacttgccgcagattgaagagcatca        398

SEQ173          258 cgtgtttcaaatccoggctgatttattgaaaaccgtgattcggcaaacgg        307
                    .|.|.|||||.|||||..-||||||.||...|..|.||.|||||.|||.
B_subtilis      399 tgccgattcagatccaactgatttgttaaaaaatctaatcagacaaacag        448

SEQ173          308 tgttcgccgtttctacatcggaaacgcgcccaatcttgacaggtgtcaac        357
                    |.||.|.||.||.||.||.||.||.||||||.||.||.||||||.|||
B_subtilis      449 tatttgcagtgtccacctcagaaacacgccctatcttgacaggtgtaaac        498

SEQ173          358 tggaaagttgaacatggcgagcttgtctgcacagcgaccgacagtcatcg        407
                    ||||||||.|.||.||.|.|..||...|.|||||.||.||.||..|||.|.
B_subtilis      439 tggaaagtggagcaaagtgaattattatgcactgcaacggatagccaccg        548
```

```
SEQ173       408 cttagccatgcgcaaagtgaaaattgagtcggaaaatgaagtatcataca   457
                 ..|.||.|..|..||.|.||!!-|!!|......|.||.-.!||.||.|
B_subtilis   549 tcttgcattaagaaaggcgaaacttgatattccagaagacagatcttata   598

SEQ173       458 acgtcgtcatccctggaaaaagtcttaatgagctcagcaaaattttggat   507
                 ||||||-||.||-|.||||||||.|-|.-|||||||||||-|||||||
B_subtilis   599 acgtcgtgattccgggaaaaagtttaactgaactcagcaagattttagat   648

SEQ173       508 gacggcaaccaaccggtggacatcgtcatgacagccaatcaagtgctatt   557
                 |||-|.|.|.|.|.||.||||.|||||.||.|.||-..|||||.||.||
B_subtilis   649 gacaaccagaaacttgtagatatcgtcatcacagaaacccaaagttctgtt   698

SEQ173       558 taaggccgagcaccttctc-ttcttttcccggctgcttgacggcaactat   606
                 ||||.|.||||..|..|.||.|||||||..|||||.|||||||.|||||
B_subtilis   699 taaag-cgaaaaacgtcttgttcttctctcacggcttctggacgggaattat   747

SEQ173       607 ccggagaacggcccgcttgattccaacagaaagcaaaacgaccatgatcgt   656
                 ||.|||.||-|||.||.|||.||.||.||.|||...||||||...|.||
B_subtilis   748 ccagacacaaccagcctgattccgcaagacagcaaaacagaaatcattgt   797

SEQ173       657 caatgcaaaagagtttctgcaggcaatcgaccggagcgtccttgcttgctc   706
                 .||..|||||||.||||.||-|.||-|.|||||||.|.|-||..|.|.||
B_subtilis   798 gaacacaaaagaattccttcaggccattgatcgtgcatctctttttagcta   847

SEQ173       707 gagaaggaaggaacaacgttgtgaaactgacgacgcttcctggaggaatg   756
                 |||||.|||-|.|||||||||-||||||.||||||.|....|||-||.|||
B_subtilis   848 gagagggacgcaacaacgttgtaaaactgtccgcaaaacc-ggctgaatc   896

SEQ173       757 c-tcgaaatttcttcgatttctcc-gagatcgggaaag-tgacggagcag   803
                 | |.|||||||||.|||||.|.|-|||||.|||||||-||.|.||||-
B_subtilis   897 cattgaaatttcttccaattcgccagaaatcggtaaagttgtggaagcaa   946

SEQ173       804 ctgcaaacggagtctcttgaagggaagagttgaacatttcgttcagcgc   853
                 .|| ...|||.....||||||||.|-|.|.|.||-||||||.|||||.|-
B_subtilis   947 ttg-ttgcggatcaaattgaaggtgaggaattaaatatctctttttagtcc   995

SEQ173       854 gaaatatatgatggacgcgttgcgggcgcttgatggaacagacatttcaa   903
                 -|.||||||||.||.||||.||.|-...||.|||||.|||.|||| |.|.-
B_subtilis   996 aaaatatatgctggatgcactaaaggtgcttgaaggagcaga-aatacgc   1044

SEQ173       904 atcagcttcactggggccatgcggccgttcctgttgcgcccgcttcaacc   953
                 -|.|||||.||.|-|.|||.||.|||-|.|||||.||.|||||.|-|..-
B_subtilis  1045 gtaagctttacaggcgcaatgagacctttcttaattcgcacgc--cgaat   1092

SEQ173       954 gat---tcgatgcttcagctcattttgccggtgagaacatat          992
                 |||   .|||.|.||||||||||.||..|.||.|.||||||.|||
B_subtilis  1093 gatgaaacgattgtacagcttatccttcctgtcagaacctattaa       1137
```

```
#=======================================
#
# Aligned_sequences: 2
# 1: SEQ173
# 2: B_licheniformis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1161
# Identity:     704/1161 (60.6%)
# Similarity:   704/1161 (60.6%)
# Gaps:         193/1161 (16.6%)
# Score: 3657.5
#
#=======================================


SEQ173             1                                    aattccgac      9
                                                        .||||||.
B_licheniform    101 aaatcgtggcctctgatgaagggtctctctgacaggcagcgattccgat    150

SEQ173            10 atttcaattgaatcgtttattccgctgaaaaagaaggcaagtt---gct     56
                     |||||.|||||||||||.||.||| .||.|||.|||.||.|||   |.|
B_licheniform    151 atttcgattgaatcgtttatcccg---aaagaagacggcgatttagagat    197

SEQ173            57 cgttg-atgtgaaaagaccggggagcatcgtactgcaggcgcgcttttc    105
                     |||..|..||||.||.|| ||.||.||.|||.|||.|||.|||||||||
B_licheniform    198 cgtgacaattgaacagccc-ggcagcattgtgcttcaagccgtttttc    246

SEQ173           106 tctgaaatcgtgaaaaaactgccgcaacaaacggtggaaatcgaaacgga    155
                     ..||||||.||.||||.|||||.|||||....|||.|||||||||....|
B_licheniform    247 agtgaaattgtcaaaaagctgccgatgtcaacagtgcaacgagggttca    296

SEQ173           156 agacaacttttgacgatcatccgctcggggcactcagaattccgcctca    205
                     |.|..|.|.||.|||||||||||||||||||.||.|..|||.||...|.|
B_licheniform    297 aaatcaatactaacgatcatccgctccggcaaagcaagtttaacttaa    346

SEQ173           206 atgggctaaacgccgacgaataatccgcgcctgcgcaaatgaagaagaa    255
                     |.||...|..|.||. ..||||||||||||||||||||||||||||||.|
B_licheniform    347 acgtttggatgcaagcgaatatccgcttttgccgcaaattgaagagcat    396

SEQ173           256 aacgtgtttcaaatcccggctgatttattgaaaaccgtgattcggcaaac    305
                     .|||.||||||||||||||||.|||.||||.|||||||.|||||.|||.|
B_licheniform    397 cacgctttcaaatccgacgatctgctgaaaaacctgatccgccaaac    446

SEQ173           306 ggtgttcgccgtttctacatcggaaacgcgcccaatcttgacaggtgtca    355
                     .||.||.|.|.||.|.|.|||.||||.|||||||||||||||||||||||
B_licheniform    447 cgtttttgcagtgtccacctcagaaacacgcccaatcttgacaggtgtaa    496

SEQ173           356 actggaaagttgaacatggc---gagcttgtctgcacagcgcgacagt    402
                     ||||||||.|| ..|| ||| ||..|..|.|||||.||||.||.||.|||
B_licheniform    497 actggaatgt--cac-tggcggtgaattaatatgcactgcaacggatagt    543
```

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SEQ173          403 catcgcttagccatgcgcaaagtgaaaattgag-tcggaa--aatgaagt   449
                    ||||     |.|.||||.||| |||||..|.|| |||..| ||.:|||.
B_licheniform   544 catc-----gtcttgcgctaag-gaaagctaagctcgacattaacgaaga   587

SEQ173          450 ---atcatacaacgtcgtcatccctggaaaaagtcttaatgagctcagca   496
                    .|||||||.||||||||||.||||||||.||||||-.|.|.|||||||||
B_licheniform   588 cagttcatacaatgtcgtcatcccaggaaaaagcttaaccgagctcagca   637

SEQ173          497 aaattttcggatgacggcaacc--acccggtggacatcgtcatgacagcca   544
                    ||||..|.|||||| ||.|. |.|..|||.||.||.||||||.|.|.|
B_licheniform   638 aaatccttgatgac--catcaggaagcttgttgatattgtgattaccgaaa   685

SEQ173          545 atcaagtgctatttaaggccgagcaccttctcttcttttcccggctgctt   594
                    .||||||||.|||||..|.|.||.|.|||||||||||.||.|.|||||||
B_licheniform   686 cacaagtgctgtttaaaacaaaaaacgttctgtttttctccaggcttctt   735

SEQ173          595 gacggcaactatccggagacggcccgcttgattccaacagaaagcaaaac   644
                    |||||    ||||||.|||.|||..|||..||||.||||||||.|||||||
B_licheniform   736 gacggaaactatccggatacgaaccgcctgattcctcaggaaagcaaaac   785

SEQ173          645 gaccatgatcgtcaatgcaaaagagtttctgcaggcaatcgacgcgagcgt   694
                    ||.|.||.||||||||||.|.||.|.|||||.|.|||.||.|||||.||
B_licheniform   786 gaacttgattgtcaatactaaggaatttctccaggcgatcgacagggctt   835

SEQ173          695 ccttgctt---gctcgagaaggaaggaacaacgttgtgaaactgacgacg   741
                    |   |||| ||..||||||||.|.||||||.||||||||...| ||
B_licheniform   836 c---gctttggcgagagaaggaacgaaacaacgtggtgaaactttc--cg   880

SEQ173          742 cttc--ctggaggaatgctcgaaatttcttcgatttctcc-gagatcggg   788
                    |..| |....|.....|.|||||||||||||||..||.||.|||||||||
B_licheniform   881 cagccgccaatgagtcgatcgaaatttcttcaaactctccggaaatcgga   930

SEQ173          789 aaag-tgacggagcagctgcaaacggagtctcttgaaggggaagagttga   837
                    ||.| ||.|||||||.|||||.|.||.|.|.||.||||||||||||||||
B_licheniform   931 aaggttgttgaaacgg-tgaatgccgagcagatcgaagggggaagacttaa   979

SEQ173          838 acatttcgttcagcgcgaaatatatgatggacgcgttgcgggcgcttgat   887
                    |.||.||||.|||||||||..|.||||||||.||.||..|...|.|||||.
B_licheniform   980 agatatcctttagtccgaaatatatgctggatgcccttaaagttcttgaa   1029

SEQ173          888 ggaacagacatttcaaatcagcttcactggggccatgcggccggtcctgt   937
                    ||||...||||| ||||.|.||||||.||.||.||.|.|.|||.|||.||
B_licheniform   1030 ggagaggaca-ttcatgtaagcttcacaggcgctagtgaggccttttctga   1078

SEQ173          938 tgcgcccgcttcaa---ccgatcgatgcttcagctcattttgccggtga   984
                    |.||.|||  |.|  .||||||||.|..|..|.|.|||.||.||.||.
B_licheniform   1079 tccgtacgc--cgaatgacgattcgatcgtccaattaattcttcctgtcc   1126

SEQ173          985 gaacatat   992
                    |.||.|||
B_licheniform   1127 ggacgtattaa   1137
```